Amendments to the Specification

Please replace the paragraph beginning at page 4, line 18 with the following rewritten paragraph:

--Both Arabidopsis and maize roots show characteristics of the closed meristem (FIGS. 23A-B ~~FIG. 23~~). However, there are important differences. In maize roots, the root apical meristem consists of three independent layers of initials. One gives rise to the stele, the second gives rise to epidermis, cortex and endodermis and the third generates the root cap, whereas in the Arabidopsis root apical meristem, the epidermis shares a common initial with the lateral root cap (Esau, K., 1977, Anatomy of Seed Plants. 2nd ed. (New York: John Wiley & Sons); Esau, K., 1953, Plant Anatomy. (New York: John Wiley & Sons)).--

Please replace the paragraph beginning at page 4, line 29 with the following rewritten paragraph:

--Primary organization of the root apical meristem in maize occurs during embryogenesis, (Steeves, T. A. and Sussex, I. M., (1989), Patterns in plant development., 2nd ed. (Cambridge University Press)) as in Arabidopsis. There are three main phases in embryo development in maize (FIGS. 24A-B ~~FIG. 24~~) (Freeling, M. and Walbot, V. (1994), The Maize Handbook, (New York: Springer-Verlag); Steeves, T. A. and Sussex, I. M. (1989), Patterns in plant development., 2nd ed., (Cambridge University Press); Sheridan, W. F. and Clark, J. K., (1993), Plant J. 3:347–358). As in Arabidopsis, the very first division of the zygote establishes the initial asymmetry of the embryo (FIG. 24A). However, unlike Arabidopsis, embryonic development in maize is characterized by rather irregular cell divisions (Sheridan, W. F. and Clark, J. K., (1993), Plant J. 3:347–358). During the first phase, the apical-basal asymmetry of the embryo is established, and the embryo is regionalized into suspensor and embryo proper (~~FIG.~~ FIGS. 24B–C). During the second phase, radial asymmetry appears and the embryonic axis and meristems are established (~~FIG.~~ FIGS. 24D–E) (Clowes, F. A. L., (1978), New Phytol. 80:409–419). Finally, during the third phase, vegetative structures such as embryonic roots and leaves are elaborated (~~FIG.~~ FIGS. 24F–G) (Sheridan, W. F. and Clark, J. K., (1993), Plant J. 3:347–358).--

Please replace the paragraph beginning at page 15, line 10 with the following rewritten paragraph:

--FIGS. 5A-1, 5A-2, 5B, 5C, 5D, 5E-1, and 5E-2 ~~FIG. 5A-E~~. Structure of the Arabidopsis *SCARECROW* gene. FIGS. 5A-1 and 5A-2 ~~FIG. 5A~~. Nucleic acid sequence and deduced amino acid sequence of the Arabidopsis *SCR* genomic region (SEQ ID NO:1) and (SEQ ID NO:2), respectively. Regulatory sequences including: (i) TATA box, (ii) ATG start codon, and (iii) potential polyadenylation sequence are underlined. Within the deduced amino acid sequence, homopolymeric repeats are underlined. FIG. 5B. Schematic diagram of genomic clone indicating possible functional motifs, T-DNA insertion sites and subclones used as probes. Abbreviations: Q,S,P,T, region with homopolymeric repeats of these amino acids; b, region with similarity to the basic region of bZIP factors; I and II, regions with leucine heptad repeats; E, acidic region. FIG. 5C. Comparison of the charged region found in Arabidopsis SCR protein with that found in bZIP transcription factors, SCR bZIP-like domain (SEQ ID NO:3), GCN4 (SEQ ID NO:4), TGA1 (SEQ ID NO:5), C-Fos (SEQ ID NO:6), c-JUN (SEQ ID NO:7), CREB (SEQ ID NO:8), Opaque–2 (SEQ ID NO:9), OBF2 (SEQ ID NO:10), RAF–1 (SEQ ID NO:11). FIG. 5D. Translations of EST clones encoding putative peptide having similarities to the VHIID domain region of Arabidopsis SCR protein (SEQ ID NO:12), F13896 (SEQ ID NO:13), Z37192 (SEQ ID NO:14), and Z25645 (SEQ ID NO:15) are from Arabidopsis, T18310 (SEQ ID NO:17) is from maize and D41474 (SEQ ID NO:16) is from rice. FIGS. 5E-1 and 5E-2 ~~FIG. 5E~~. The deduced amino acid sequence of the Arabidopsis *SCARECROW* gene (SEQ ID NO:2).--

Please replace the paragraph beginning at page 17, line 3 with the following rewritten paragraph:

--FIGS. 8A-B ~~FIG. 8~~. Partial nucleotide sequence (SEQ ID NO:18) and deduced amino acid sequence (SEQ ID NO:19) of the Arabidopsis *SCLa4* gene.--

Please replace the paragraph beginning at page 17, line 6 with the following rewritten paragraph:

--FIGS. 9A-B ~~FIG. 9~~. Partial nucleotide sequence (SEQ ID NO:20) and deduced amino acid sequence (SEQ ID NO:21) of the Arabidopsis *SCLa3* gene.--

Please replace the paragraph beginning at page 17, line 14 with the following rewritten paragraph:

--FIGS. 11B1 and 11B2 ~~FIG. 11B~~. Partial nucleotide sequence (SEQ ID NO:26) and deduced amino acid sequence (SEQ ID NO:27) of the maize *SCLm1* gene (Zm–Sc12).--

Please replace the paragraph beginning at page 18, line 29 with the following rewritten paragraph:

--FIGS. 17A-1 and 17A-2 ~~FIG. 17A~~. The partial nucleotide sequence (SEQ ID NO.66) of the maize *ZCR* gene.--

Please replace the paragraph beginning at page 19, line 18 with the following rewritten paragraph:

--FIGS. 19A-G ~~FIG. 19~~. Comparison of promoter activities in transgenic lines and roots. FIG. 19A ~~Panel a~~. A stably transformed line containing four copies of the B2 subdomain of the 35S promoter of CaMV upstream of GUS (Benfey et al., 1990). GUS is expressed in the root tip. FIG. 19B ~~Panel b~~. Roots emerging from callus transformed with four copies of the B2 subdomain of the 35S promoter fused to GUS. GUS expression can be seen in the emerging root tips (arrows). FIG. 19C ~~Panel c~~. Higher magnification of a root emerging from the callus in FIG. 19B ~~panel b~~. GUS is clearly restricted to the root tip. The morphology of roots regenerated from calli often appears abnormal. FIG. 19D ~~Panel d~~. A transgenic plant regenerated from the calli and roots shown in FIG. 19B ~~panel b~~. GUS expression in this plant ~~plants~~ appears to be similar to that of the original line shown in FIG. 19A ~~panel a~~. FIG. 19E ~~Panel e~~. ET199, a stably transformed line that contains an enhancer trapping construct with a minimal promoter fused to the GUS coding region inserted 1 kb upstream from the *SCR* coding region. GUS expression is primarily in the endodermal layer of the root. FIG. 19F ~~Panel f~~. Roots emerging from calli transformed with the *SCR* promoter::GUS construct. Expression of the GUS gene appears to be limited to an internal layer (arrows). FIG. 19G ~~Panel g~~. *SCR* promoter::GUS transformed root in liquid culture. Roots shown in FIG. 19F ~~panel f~~ were excised and transferred to liquid cultures. GUS

expression is primarily found in the endodermal layer as in ET199. The expression of GUS in the quiescent center, as seen here, is also sometimes observed in ET199. Bar, 50μm.--

Please replace the paragraph beginning at page 20, line 10 with the following rewritten paragraph:

--FIGS. 20A-B ~~FIG. 20~~. Analysis of *SCR* promoter activity in the *scr* mutant background. FIG. 20A ~~**Panel a**~~. Roots emerging from *scr* calli transformed with the *SCR* promoter::GUS construct. Roots regenerated from *scr* calli are very short. GUS expression appears to be limited to an internal layer of the root (arrows). FIG. 20B ~~**Panel b**~~. Root regenerated from transformed *scr* calli and transferred to liquid culture. The *scr* phenotype, a single layer between the epidermis and pericycle, is easily seen. GUS expression is limited to this mutant layer. E, Epidermis. M, Mutant Layer. P, Pericycle. Bar, 50μm.--

Please replace the paragraph beginning at page 20, line 21 with the following rewritten paragraph:

--FIGS. 21A-F ~~FIG. 21~~. Molecular Complementation of the *scr* mutant. FIGS. 21A, 21C, and 21E ~~**Panels a, c and e**~~. *scr* transformed with the *SCR* promoter::GUS construct. FIGS. 21B, 21D, and 21F ~~**Panels b, d and f**~~. *scr* transformed with the *SCR* promoter::*SCR* coding region construct. FIGS. 21A and 21B ~~**Panels a and b**~~. Roots emerging from *scr* calli. Arrows point to several very short roots among many fine root hairs in the *scr* calli transformed with the *SCR* promoter::GUS construct. In contrast, roots from *scr* calli transformed with the *SCR* promoter::*SCR* coding region construct appeared to be wild-type in length, suggesting molecular complementation by the transgene. FIGS. 21C and 21D ~~**Panels c and d**~~. Transgenic roots in liquid culture. The *scr* roots transformed with the *SCR* promoter::GUS construct appeared short, while those transformed with the *SCR* promoter::*SCR* coding region construct appeared of wild-type length. FIGS. 21E and 21F ~~**Panels e and f**~~. Transverse sections through roots emerging from calli. Whereas there is only a single cell layer between the epidermis and stele in the *SCR* promoter::GUS transformed root, the radial organization of the root transformed with the *SCR* promoter::*SCR* coding region appeared identical to wild-type, with both cortex and endodermal layers. E, epidermis. M, mutant layer. C, cortex. En, Endodermis. P, Pericycle. Bar, 50μm.--

Please replace the paragraph beginning at page 22, line 3 with the following rewritten paragraph:

--FIGS. 25A-C ~~FIG.25A-B~~. Maize Scarecrow gene. The nucleotide (SEQ ID NO:95) and deduced amino acid sequence (SEQ ID NO:96) of the maize scarecrow gene *(ZCR)* is shown (SEQ ID NOS:95-98). The amino acid numbers are shown on the right, while the nucleotides are numbered on the left.--

Please replace the paragraph beginning at page 22, line 7 with the following rewritten paragraph:

--FIGS. 26A-1 and 26A-2 ~~FIG. 26A~~. Amino acid sequence alignment of maize *ZCR* (SEQ ID NO: 96) and Arabidopsis *SCR* (SEQ ID NO:2). Identical residues are marked by asterisks. In addition, three copies of an LXXLL motif are underlined.--

Please replace the paragraph beginning at page 22, line 11 with the following rewritten paragraph:

--FIGS. 27A-H ~~27A-G~~. Maize Scarecrow gene expression during regeneration of the root apex following excision of the QC. FIGS. 27A–B. Immediately after removal of the root cap and excision of the QC, no significant alteration in the expression pattern was observed. FIGS. 27C–D. Maize expression pattern 24 hours following excision of the QC. These figures show isolated expression of the gene between cell files. FIG. 27E. Expression 48 hours following excision of the QC. This figure shows that the root tip has regained much of its normal shape, although the cell files have not organized into the converging files seen in normal roots. FIG. 27F. Expression 72 hours following excision of the QC. At this stage, the expression pattern resembles that found in the unexcised root. FIG. 27G. Expression 96 hours following excission of the QC. At this stage, the expression pattern is similar to that seen in the primary root.--

Please replace the paragraph beginning at page 22, line 27 with the following rewritten paragraph:

--FIGS. 28 and 28A-1 to 28A-33 ~~28A–AH~~. The partial nucleotide and amino acid sequences (SEQ ID NOS:68-94) of Arabidopsis EST's that encode members of the

SCARECROW-like *(SCL)* gene family (SEQ ID NOS: 68-94, 23, 21, 19, 46, 50, 54, and 58 respectively). "N" indicates an unknown base.--

Please replace the paragraph beginning at page 22, line 32 with the following rewritten paragraph:

--FIGS. 29A-C ~~FIG. 29~~. Alignment of the Arabidopsis GRAS gene products (SCL3 (SEQ ID NO: 21), SCL11 (SEQ ID NO: 50), SCL9 (SEQ ID NO: 113), SCL14 (SEQ ID NO: 58), SCL16 (SEQ ID NO: 126), SCL13 (SEQ ID NO: 54), SCL5 (SEQ ID NO: 128), SCL1 (SEQ ID NO: 23), SCL8 (SEQ ID NO: 116), SCL4 (SEQ ID NO: 117), SCL7 (SEQ ID NO: 52), SCL6 (SEQ ID NO: 46; residues 21-378), SCL15 (SEQ ID NO: 119), SCL18 (SEQ ID NO: 120), GAI (SEQ ID NO: 150), RGA (SEQ ID NO: 149), RGAL (SEQ ID NO: 123), SCL 19 (SEQ ID NO: 130 and SCR (SEQ ID NO: 2)). The highly conserved region of the GRAS products can be divided into five recognizable motifs, indicated in the figure. *See also,* for example, Section 5.1.5., *infra*. The absolutely conserved residues within the VHIID (SEQ ID NO: 145) and SAW (SEQ ID NO: 146) motifs are highlighted in bold, as are the hydrophobic residues of the leucine heptads, the P-F-Y-R-E residues of the PFYRE motif (SEQ ID NO: 147), and the two short sequences that define the end of the VHIID motif (SEQ ID NO: 145) and the beginning of the PFYRE motif (SEQ ID NO: 147). The @ symbol in the alignment indicates the location of an apparent insertion in the *SCL3* gene (SEQ ID NO: 148). The deduced amino acid sequence of the insertion is shown at the bottom of the figure.--

Please replace the paragraph beginning at page 23, line 22 with the following rewritten paragraph:

--FIGS. 31A-D ~~FIG. 31~~. *In situ* Hybridizations with *SCR* and *SCL3*. Transverse sections (FIGS. 31A, 31B, and 31D ~~a, b, and d~~) and a longitudinal section (FIG. 31C ~~c~~) of 7 day old roots were hybridized with either an antisense *SCR* riboprobe (FIG. 31A ~~a~~), an antisense *SCL3* riboprobe (FIGS. 31B and 31C ~~b and c~~) or a sense *SCL3* riboprobe (FIG. 31D ~~d~~). Strong signal is observed in the endodermis with the antisense *SCR* probe and the antisense *SCL3* probe, but not with the sense *SCL3* probe. Scale bars in FIGS. 31A and 31C ~~(a) and (c)~~ are both 25 mm. The magnification is the same in FIGS. 31A, 31B, and 31D ~~panels (a), (b), and (d)~~.--

Please replace the paragraph beginning at page 24, line 1 with the following rewritten paragraph:

--FIGS. 33A-B ~~FIG. 33~~. CBPBTT44 Partial cDNA (SEQ ID NO: 104) and Amino Acid Sequence (SEQ ID NO: 105). The partial nucleotide and amino acid sequence of CBPBTT44, a closely related gene to the maize *ZCR* gene.--

Please replace the paragraph beginning at page 26, line 30 with the following rewritten paragraph:

--The *SCARECROW* genes and nucleotide sequences of the invention include: (a) a gene listed below in Tables 1 or 2 (hereinafter, a gene comprising any one of the nucleotide sequences shown in FIG. 5A-1, FIG. 5A-2, FIGS. 8A-B, FIGS. 9A-B, FIG.10, FIG. 11A, FIG. 11B1, FIG. 11B2, FIGS. 12A-B, FIGS. 16A-E, FIG. 16F-1, FIG. 16F-2, FIGS. 16G-I, FIG. 16J-1, FIG. 16J-2, and FIGS. 16K-M ~~FIG. 5A, FIG. 8, FIG. 9, FIG. 10, FIGS. 11A-B, FIGS. 12A-B, FIGS. 16A-M, FIG. 17A, FIG. 25 or FIGS. 28A-AH~~, or a segment of such nucleotide sequences), or as contained in the clones described herein and deposited with the ATCC (see Section 13, infra); (b) a nucleotide sequence that encodes a protein comprising any one of the amino acid sequences shown in FIG. 5A-1, FIG. 5A-2, FIG. 5D, FIG. 5E-1, FIG. 5E-2, FIGS. 8A-B, FIGS. 9A-B, FIG. 11A, FIG. 11B1, FIG. 11B2, FIGS. 13A-F, FIGS. 15A-S, FIG. 17B, FIG. 18, or FIGS. 25A-C ~~FIG. 5A, FIG. 5D, FIG. 5E, FIG. 8, FIG. 9, FIGS. 11A-B, FIGS. 13A-F, FIGS. 15A-S, FIG. 17B, FIG. 18 or FIG. 25~~, or a segment of such amino acid sequences, or that is encoded by any one of the genes and/or nucleotide sequences listed by their sequence identifier numbers in Tables 1 or 2, or any segment of such genes and/or nucleotide sequences, or contained in any one of the clones described herein and deposited with the ATCC (see section 13, infra); (c) any gene comprising a nucleotide sequence that hybridizes to the complement of any one of the genes and/or nucleotide sequences listed by their sequence identifier numbers in Tables 1 or 2, or any segment of such genes and/or nucleotide sequences, or as contained in any one of the clones described herein and deposited with the ATCC, under highly stringent conditions, *e.g.*, hybridization to filter-bound DNA in 0.5 M $NaHPO_4$, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1xSSC/0.1% SDS at 68°C (Ausubel F.M. et al., eds., 1989, Current Protocols in Molecular Biology, Vol. I, Green Publishing Associates, Inc., and

John Wiley & Sons ~~sons~~, Inc., New York, at p. 2.10.3) and that encodes a gene product functionally equivalent to *SCR* gene product encoded completely or partly by any one of the genes and/or sequences listed in Tables 1 or 2 or any segment of such genes and nucleotide sequences, or as contained in any one of the clones deposited with the ATCC; (d) any gene comprising a nucleotide sequence that hybridizes to the complement of any one of the sequences listed by their sequence identifier numbers in Tables 1 or 2, or any segment of such nucleotide sequences, or as contained in any one of the clones described herein and deposited with the ATCC, under less stringent conditions, such as moderately stringent conditions, *e.g.*, washing in 0.2xSSC/0.1% SDS at 42°C (Ausubel et al., 1989, *supra),* and which encodes a functionally equivalent *SCR* gene product; (e) any gene comprising a nucleotide sequence that hybridizes to the complement of any one of the sequences listed by their sequence identifier numbers in Tables 1 or 2 or any segment of such nucleotide sequences, or as contained in any one of the clones described herein and deposited with the ATCC, under the following low stringency conditions: pre-hybridization in hybridization solution (HS) containing 43% formamide, 5xSSC, 1% SDS, 10% dextran sulfate, 0.1% sarkosyl, 2% block (Genius kit, Boehringer-Mannheim), followed by hybridization overnight at 30 to 33°C using as a probe a DNA molecule of approximately 1.6 kb of SEQ ID NO:1 at a concentration of 20 ng/ml, followed by washing in 2xSSC/0.1% SDS two times for 15 minutes at room temperature and then two times at 50°C, and which encodes a functionally equivalent *SCR* gene product; and/or (f) any gene comprising a nucleotide sequence that encodes a polypeptide or protein containing the consensus sequence for SCR (*i.e.*, MOTIF III or VHIID) shown in FIGS. 13B–D or a segment of such polypeptide or protein. The partial and complete nucleotide and amino acid sequences of SCR genes and encoded proteins and polypeptides included in the invention are listed in Tables 1 or 2 below.--

Please replace footnote 3 of Table 1 beginning at page 30, line 20 with the following rewritten footnote 3:

--[3] The partial or complete nucleotide sequence of the *SCR* orthologs and paralogs listed here are shown in FIGS. 5A-1, 5A-2, 8A-B, 9A-B, 10, 11A, 11B1, 11B2, 12A-B, 16A-E, 16F-1, 16F-2, 16G-I, 16J-1, 16J-2, 16K-M, 17A1, 17A-2, and 25A-C ~~FIGS. 5A, 8, 9, 10, 11A–B, 12A–B, 16A–M, 17A and 25.~~--

Please replace the paragraph beginning at page 34, line 4 with the following rewritten paragraph:

--In particular, the invention includes, for example, fragments of *SCR* genes encoding one or more of the following domains as shown in FIGS. 5E-1 and 5E-2 ~~FIG. 5E~~: amino acids 1–264, 265–283, 287–316, 410–473, 436–473, and 473–653.--

Please replace the paragraph beginning at page 34, line 18 with the following rewritten paragraph:

--A specific embodiment of a *SCR* gene and coding sequence of the invention is Arabidopsis *SCR* (FIGS. 5A-1, 5A-2, 5E-1, and 5E-2 ~~5A and 5E~~). Other specific embodiments include the various *SCR* genes and coding sequences listed in Tables 1 or 2, *supra.*--

Please replace the paragraph beginning at page 38, line 30 with the following rewritten paragraph:

--An *SCR* or *SCL* gene coding sequence also may be isolated by screening a plant genomic or cDNA library using an *SCR* or *SCL* nucleotide sequence (*e.g.*, the sequence of any of the *SCR* or *SCL* genes and sequences and EST clone sequences listed in Table 1 and Table 2.) as a hybridization probe. For example, the whole, or a segment, of the Arabidopsis *SCR* nucleotide sequence (FIGS. 5A-1 and 5A-2 ~~FIG. 5A~~) may be used. Alternatively, a *SCR* or *SCL* gene may be isolated from such libraries using a degenerate oligonucleotide that corresponds to a segment of a SCR amino acid sequence as a probe. For example, a degenerate oligonucleotide probe corresponding to a segment of the Arabidopsis SCR amino acid sequence (FIGS. 5E-1 and 5E-2 ~~FIG. 5E~~) may be used.--

Please replace the paragraph beginning at page 40, line 20 with the following rewritten paragraph:

--The identity of a cloned or amplified *SCR* gene sequence can be verified by comparing the amino acid sequences of its three open reading frames with the amino acid sequence of a *SCR* gene *(e.g.,* Arabidopsis SCR protein [SEQ ID NO:2]). A *SCR* gene or coding sequence encodes a protein or polypeptide whose amino acid sequence is substantially similar to that of a SCR protein or polypeptide (*e.g.,* the amino acid sequence of any one of

the SCR proteins and/or polypeptides shown in FIGS. 5A-1, 5A-2, 5E-1, 5E-2, 8A-B, 9A-B, 11A, 11B1, 11B2, 15A-S, 17B, 18, and 25A-C ~~FIG. 5A, 5E, FIG. 8, FIG. 9, FIGS. 11A-B, FIGS. 15A-S, FIG. 17B, FIG. 18 and FIG. 25~~). The identity of the cloned or amplified *SCR* gene sequence may be further verified by examining its expression pattern, which should show highly localized expression in the embryo and/or root of the plant from which the *SCR* gene sequence was isolated.--

Please replace the paragraph beginning at page 49, line 31 with the following rewritten paragraph:

--Scarecrow-like *(SCL)* genes are genes which show a high degree of similarity to the *SCR* gene. Tables 1 and 2 show a list of various *SCL* genes which were recently identified. Tables 1 and 2 also show each EST clone and/or genomic sequence corresponding with each of the *SCL* genes. The partial nucleotide sequence of various Arabidopsis EST's that encode members of the *SCL* gene family are shown in FIGS. 28 and 28A-1 to 28A-33 ~~28A-AH~~.--

Please replace the paragraph beginning at page 50, line 4 with the following rewritten paragraph:

--Sequence analysis of the genes showed that a variable amino-terminal (N-terminal) and a highly conserved carboxyl-termini (C-termini) region exist throughout these putative gene products. The highly conserved region does not show significant similarity to members of any recognized gene family, indicating that these sequences likely define a novel gene family. Based on the high degree of similarity of the gene products to *SCR,* the genes corresponding to these ESTs were designated SCARECROW-LIKE *(SCL).* Recently, the importance of this gene family has been confirmed. Two components of the gibberellin signal transduction pathway, the gene products of the GIBBERELLIN-ACID INSENSITIVE (GAI) and the REPRESSOR OF GA1 (RGA) loci, have been shown to be members of this family (Peng et al., 1997, Genes & Dev. 11, 3194–3205; Silverstone et al., 1998, Plant Cell 10, 155-169). Thus, this family of gene products has been designated as the GRAS gene family, an acronym based on the designations of the known genes: GAI, RGA and SCR. An alignment of various GRAS gene products is shown at FIGS. 29A-C ~~FIG. 29~~. As shown on the figure, the gene products have at least five recognizable motifs that are

highly conserved. The absolutely conserved residues within the VHIID and SAW motifs are highlighted in bold, as are the hydrophobic residues of the leucine heptads, the P-F-Y-R-E residues of the PFYRE motif, and the two short sequences that define the end of the VHIID motif and the beginning of the PFYRE motif.--

Please replace the paragraph beginning at page 50, line 30 with the following rewritten paragraph:

--The GRAS family includes at present nineteen distinct members in Arabidopsis: fifteen SCLs, SCR, GAI, RGA, and RGAL (a GRAS sequence of unknown function with high similarity to GAI and RGA). The fact that the SCR, GAI, and RGA gene products have diverse roles in fundamental processes in plant biology (SCR in pattern formation and GAI/RGA in signal transduction) suggests that other members of this family may also play important roles in the physiology and development of higher plants. Intriguingly, the majority of the *SCL* genes are expressed predominantly in the root. FIG. 30 and Table 3. Furthermore, one of these (*SCL3*) has an expression pattern in the root that is similar to that of *SCR*. FIGS. 31A-D ~~FIG. 31~~. In addition to root, many of the *SCL* genes are expressed in siliques and shoots. *See*, Table 3.--

Please replace the paragraph beginning at page 53, line 2 with the following rewritten paragraph:

--According to the present invention, *SCR* promoters and functional portions thereof described herein refer to regions of the *SCR* gene which are capable of promoting tissue-specific expression in embryos, roots and shoots of an operably linked coding sequence in plants. The *SCR* promoter described herein refers to the regulatory elements of *SCR* genes, *i.e.*, regulatory regions of genes which are capable of selectively hybridizing to the nucleic acids described in Section 5.1, or regulatory sequences contained, for example, in the region between the translational start site of the Arabidopsis *SCR* gene and the HindIII site approximately 2.5 kb upstream of the site in plasmid pLIG1-3/SAC+Mob21SAC (see FIGS. 5A-1, 5A-2, ~~5A~~ and 14) in hybridization assays, or which are homologous by sequence analysis (containing a span of 10 or more nucleotides in which at least 50 percent of the nucleotides are identical to the sequences presented herein). Homologous nucleotide sequences refer to nucleotide sequences including, but not limited to, *SCR* promoters in

diverse plant species *(e.g.,* promoters of orthologs of Arabidopsis *SCR)* as well as genetically engineered derivatives of the promoters described herein.--

Please replace the paragraph beginning at page 55, line 12 with the following rewritten paragraph:

--According to the present invention, a *SCR* promoter is one that confers to an operably linked gene in a transgenic plant tissue-specific expression in roots, root nodules, stems and/or embryos. A *SCR* promoter comprises the region between about -5,000 bp and +1 bp upstream of the transcription initiation site of a *SCR* gene. In a particular embodiment, the Arabidopsis *SCR* promoter comprises the region between positions -2.5 kb and +1 in the 5' upstream region of the Arabidopsis *SCR* gene (see FIGS. 5A-1, 5A-2, ~~5A~~ and 14).--

Please replace the paragraph beginning at page 57, line 20 with the following rewritten paragraph:

--The present invention provides for use of recombinant DNA constructs which contain tissue-specific and developmental-specific promoter fragments and functional portions thereof. As used herein, a functional portion of a *SCR* promoter is capable of functioning as a tissue-specific promoter in the embryo, stem, root nodule and/or root of a plant. The functionality of such sequences can be readily established by any method known in the art. Such methods include, for example, constructing expression vectors with such sequences and determining whether they confer tissue-specific expression in the embryo, stem, root nodule and/or root to an operably linked gene. In a particular embodiment, the invention provides for the use of the Arabidopsis *SCR* promoter contained in the sequences depicted in FIGS. 5A-1, 5A-2, ~~5A~~ and 14 and the insert DNA of plasmid pGEX–2TK^{+}.--

Please replace the paragraph beginning at page 72, line 20 with the following rewritten paragraph:

--A probe made from a rescued fragment of 1.2 kb was used to screen a wild-type genomic library made from WS plants. One genomic clone containing an insert of approximately 23 kb was isolated. A 3.0 kb Sac I fragment from the genomic clone, which hybridized to the 1.2 kb probe, was subcloned and sequenced (FIGS. 5A-1 and 5A-2 ~~FIG. 5A~~). Comparison of the nucleotide sequence between the genomic clone and the

rescued plasmid revealed the site of the T-DNA insertion. Approximately 600,000 plaques from a cDNA library, obtained from inflorescences and siliques (Col ecotype), and therefore enriched in embryos, were screened with the 1.2 kb probe. Four cDNA clones were isolated. The dideoxy sequencing method was performed using the Sequenase kit (United States Biochemical Corp.). Sequence-specific internal primers were synthesized and used to sequence the Sac I genomic as well the cDNA clones. Total RNA from plant tissues was obtained using phenol/chloroform extractions as described in Berry et al., 1985, Mol. Cell. Biol. 5:2238–2246 with minor modifications. Northern hybridization and detection were performed according to the Genius kit manual (Boehringer Mannheim).--

Please replace the paragraph beginning at page 78, line 2 with the following rewritten paragraph:

--To further elucidate the function of the Arabidopsis *SCR* gene, the inserted T-DNA sequences were used to clone the gene. Plant DNA flanking the insertion site was obtained from *scr–1* by plasmid rescue and used to isolate the corresponding wild-type genomic DNA. Several cDNA clones were isolated from a library made from silique tissue. Comparison of the sequence of the longest cDNA and the corresponding genomic region revealed an open reading frame (ORF) interrupted by a single small intron. (FIGS. 5A-1 and 5A-2 ~~FIG. 5A~~). A potential TATA box and polyadenylation signal that matched the consensus sequences for plant genes were also identified (Joshi, C.P., 1987, Nucl. Acids Res. 15:6643–6653); Heidecker & Messing, 1986, Ann. Rev. Plant Physiol. 37:439–466); Mogen et al., 1990, Plant Cell 2:1261–1272).--

Please replace the paragraph beginning at page 78, line 16 with the following rewritten paragraph:

--Comparison of the nucleotide sequence between the genomic clone and the rescued plasmid placed the site of the T-DNA insertion in *scr–1* at codon 470 (FIGS. 5A-1, 5A-2, ~~5A~~ and 5B). For *scr–2*, although no linkage was found between the mutant phenotype and antibiotic resistance, DNA blot and PCR analysis of antibiotic sensitive lines revealed the presence of T-DNA sequences that co-segregated with the mutant phenotype. The insertion position in *scr–2* was determined by cloning and sequencing the PCR products amplified from its genomic DNA using a combination of T-DNA and *SCR* specific primers at both

sides of the insertion (FIG. 5B). In *scr–2*, the T-DNA insertion point is at codon 605 (FIGS. 5A-1, 5A-2, ~~FIG. 5A~~ and 5B).--

Please replace the paragraph beginning at page 86, line 18 with the following rewritten paragraph:

--Analysis of at least eighteen EST clones found in the GenBank database reveals that the proteins they encode share a high degree of homology with Arabidopsis SCR protein. See Tables 1 and 2 and FIGS. 15A–S, 28, and 28A-1 to 28A-33 ~~and 28A–AH~~. Further sequence analysis of the encoded proteins indicate that a high degree of sequence similarity extends from at least the highly conserved VHIID domain to the carboxy-terminus of the gene products. Comparison of the amino termini of these proteins is precluded by the fact that the ESTs are incomplete. The high degree of similarity among these proteins, in combination with the motifs observed in the SCR protein (homopolymeric motifs, two leucine heptad repeats and a bZIP-like basic domain that may also function as a nuclear localization sequence) indicates that these proteins form a novel class of regulatory proteins.--

Please replace the paragraph beginning at page 95, line 25 with the following rewritten paragraph:

--A large number of roots were regenerated. They show GUS staining pattern that is similar to the *SCR* expression pattern in ET199 plants (FIG. 19F ~~Figure 19, Panel f~~). Since organs regenerated from callus often have an abnormal morphology, transgenic roots were transferred to liquid culture. Roots grown in liquid culture appeared morphologically normal and showed GUS expression in the endodermis, endodermal initial and QC (FIG. 19G ~~Panel g~~), similar to the expression pattern of *SCR* seen in the enhancer trap line ET199. These results indicate that the 2.5 kb region upstream of the *SCR* start site is sufficient to confer the *SCR* expression pattern in the root.--

Please replace the paragraph beginning at page 96, line 9 with the following rewritten paragraph:

--Transgenic roots of the *scr* mutant that contained a *SCR* promoter::GUS construct were generated. As in the wild-type, a large number of transgenic roots were

formed that had detectable GUS expression (FIG. 20A ~~Figure 20, Panel a~~). These roots were shorter than wild-type regenerated roots, consistent with the shorter root phenotype of the *scr* mutant.--

Please replace the paragraph beginning at page 96, line 15 with the following rewritten paragraph:

--Additional transgenic root experiments demonstrated that the *SCR* gene under control of its own promoter can rescue the *scr* mutant phenotype. Transgenic *scr* roots were generated that contained the full length *SCR* gene under the control of its own promoter. The length of transgenic roots containing the construct were longer than those of the *scr* mutant, indicating that the introduced *SCR* gene partially rescued the mutant. Whereas *scr* regenerated roots that carried the *SCR* promoter::GUS construct were very short (FIG. 21A ~~Figure 21, Panel a~~; and FIG. 20A ~~Figure 20, Panel a~~), roots transformed with the *SCR* promoter and coding region were noticeably longer (FIG. 21B ~~Figure 21, Panel b~~). The difference was even more obvious in liquid culture, in which *scr* mutant roots remained short (FIG. 21C ~~Figure 21, Panel c~~), while *SCR* gene complemented *scr* mutant roots were long and resembled wild-type roots (FIG. 21D ~~Figure 21, Panel d~~).--

Please replace the paragraph beginning at page 96, line 31 with the following rewritten paragraph:

--Anatomical studies of the regenerated roots confirmed the ability of the *SCR* promoter::*SCR* gene construct to rescue the *scr* mutant phenotype. Whereas regenerated roots of *scr* mutants were missing an internal layer (FIG. 21E ~~Figure 21, Panel e~~), the *scr* mutant roots that were transformed with the *SCR* promoter::*SCR* gene construct had a radial organization that resembled wild-type root (FIG. 21F ~~Figure 21, Panel f~~).--

Please replace the paragraph beginning at page 98, line 7 with the following rewritten paragraph:

-- A positive clone was identified. The clone contained a 13 kb insert, which was subcloned into a plasmid vector. The resulting plasmid was designated pZCR. A 5 kb Eco RI fragment containing the maize *SCR* (*ZCR*) sequence was subcloned and sequenced. The nucleotide sequence of the region containing a partial *ZCR* coding sequence is shown in

FIGS. 17A-1 and 17A-2 ~~FIG. 17A~~ and the corresponding deduced amino acid sequence is shown in FIG. 17B. The ZCR protein contains a segment that is highly homologous to a corresponding segment in the Arabidopsis SCR protein (FIG. 17B). This segment is flanked by segments of low homology. Thus, it is possible that the genomic clone of ZCR is a composite clone, containing sequences that are not ZCR sequences.--

Please replace the paragraph beginning at page 99, line 31 with the following rewritten paragraph:

--The results show that *ZCR* expression in maize primary roots is localized to a file of cells that is identified as the endodermal layer. The expression pattern continues in a single uninterrupted file through the QC which consists of approximately 1000-1500 cells (FIGS. 22A-F ~~FIG. 22~~).--

Please replace the paragraph beginning at page 102, line 23 with the following rewritten paragraph:

--Subsequently, a 5kb SalI fragment from one of the three clones was subcloned into pBluescript SK(-) and sequenced. The sequence analysis of the cloned maize gene revealed that it consists of two exons and one intron in one open-reading frame (ORF) encoding 668 amino acids. The presence of an in-frame stop codon located 5' to the initiating ATG and nearby stop codons in the other two reading frames suggests that the long ORF of this genomic clone encodes the functional, full length protein. *See*, FIGS. 25A-C ~~FIG. 25~~.--

Please replace the paragraph beginning at page 102, line 33 with the following rewritten paragraph:

--After obtaining the full length maize sequence, a database search was performed to find homologous sequences. The database search revealed that the newly isolated maize sequence was most homologous with the Arabidopsis *SCR* gene at the amino acid level. Comparison of the maize and Arabidopsis sequences indicated that the similarity between the Arabidopsis *SCR* and the maize *ZCR* gene extended beyond the VHIID domain into both the N- and C-termini (FIGS. 26A-1 and 26A-2 ~~FIG. 26~~). Although the N-terminal region of the maize ortholog and the Arabidopsis *SCR* gene appears wore divergent, the

maize *ZCR* gene has the homopolymeric stretches characteristic of *SCR* (Gerber et al., 1994, Science 263:808–811; Johnson, et al., 1993, J. Nutr. Biochem. 4:386-398).--

Please replace the paragraph beginning at page 103, line 11 with the following rewritten paragraph:

--In addition, the *ZCR* gene has other motifs characteristic of *SCR*: two putative leucine heptad repeats, which have been shown in other proteins to mediate protein-protein interactions; and a stretch of basic residues similar to the basic domain of bZIP proteins, which have been shown not only to mediate DNA-binding, but also nuclear localization (Hurst, H.C., 1994, Protein Prof. 1:123–168). Moreover, the *ZCR* gene has three copies of an LXXLL motif in the N-terminal region, which has been shown to mediate the binding of a steroid receptor coactivator complex to nuclear receptors (Heery, et al., 1997, Nature 387:733–736; Torchia, et al., 1997, Nature 387:677–684). *See*, FIGS. 26A-1 and 26A-2 ~~FIG. 26~~. Similarly, the GAI and RGA gene products also contain a copy of this sequence. In these genes, the sequence is believed to be involved in a gibberellin signal transduction pathway (Peng, et al., 1997, Genes Dev. 11:3194–3205; Silverstone, et al., 1998, Plant Cell 10:155–169).--

Please replace the paragraph beginning at page 104, line 15 with the following rewritten paragraph:

--FIGS. 33A-B ~~FIG 33~~ shows the partial nucleic acid and amino acid sequence of CBPBT44, a gene which has significant homology to both the Arabidopsis *SCR* and the maize *ZCR* genes. FIG. 34 represents an alignment of the three genes. As shown in FIG. 34, the three genes share a high degree of homology, including, but not limited to, the leucine heptad repeats. To further demonstrate the homology between the maize *ZCR* gene and the CBPBT44 partial sequence, a Southern blot analysis was performed. *See*, FIG. 35. FIG. 35 demonstrates that CBPBT44 (right pane, lane C) is the source of some of the bands picked up by the maize *ZCR* cDNA (right panel, lane A). Thus, it is likely that CBPBT44 is a closely related gene to the *ZCR* gene, and that CBPBT44 may represent a duplicated copy of the maize *ZCR* gene in the maize genome. This possibility is strengthened by the fact that maize is thought to have undergone a general duplication of its genome during its evolution.--

Please replace the paragraph beginning at page 105, line 2 with the following rewritten paragraph:

--In order to understand the function of the maize *ZCR* ortholog, the expression pattern of the maize ortholog was examined in various types of roots, including, but not limited to, the maize primary, embryonic, lateral, seminal lateral and adventitious roots by RNA *in situ* hybridization. Surprisingly, in spite of the profound differences of the root architecture between maize and Arabidopsis (FIGS. 23A-B ~~FIG. 23~~), the expression pattern of the maize *ZCR* is remarkably similar to that of the Arabidopsis *SCR* in that expression is found only in the endodermis cell lineage (FIGS. ~~Fig.~~ 22A–C). Furthermore, it is expressed in the embryonic root and lateral root (FIGS. ~~FIG.~~ 22D–F).--